

**Amendment and Listing of the Claims**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

Claims 1-52. (cancelled)

Claim 53. (new) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed in soybean, produces an RNA having:

- (a) homology to at least one target mRNA expressed in soybean, and
- (b) two fully complementary RNA regions which are unrelated to any endogenous RNA in the host and which are transcribed from SEQ ID NO:13 , comprising at least nucleotides 7-36 and 82-111 or 7-36, 44-73, 82-111 and 119-148 of SEQ ID NO: 13, and which are in proximity to a sequence homologous to all or part of the RNA in (a), wherein the recombinant construct, when expressed in soybean reduces expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the RNA in (a) based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 54. (new) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed in soybean, produces an RNA having:

- (a) homology to at least one target mRNA expressed in soybean,
- (b) an RNA region which is unrelated to any endogenous RNA in the host and which is transcribed from SEQ ID NO:13, comprising at least nucleotides 7-36 or 7-36 and 44-73 and is located 5' to a sequence homologous to all or part of the RNA in (a), and
- (c) the reverse complement of (b), comprising at least nucleotides 82-111 or 82-111 and 119-148 and is located 3' to a sequence homologous to all or part of the RNA in (a), further wherein the recombinant construct expressed by the host

reduces the expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the RNA described in (a) based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 55. (new) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed in soybean, produces an RNA having:

- (a) homology to at least one target mRNA expressed in soybean, and
- (b) two fully complementary RNA regions, which are unrelated to any endogenous RNA in soybean, which are transcribed from SEQ ID NO:13, said SEQ ID NO:13 comprising a NotI site, and which are in proximity to a sequence homologous to all or part of the RNA in (a), wherein said DNA sequence is introduced into the NotI site of SEQ ID NO:13 and wherein the recombinant construct, when expressed in soybean reduces expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the RNA in (a) based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 56. (new) A method for reducing expression of a target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of RNA homologous to a target mRNA expressed in soybean based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4, the method comprising:

- (a) transforming soybean with any of the recombinant constructs of Claims 46-47; and

(b) selecting soybean which have reduced expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the RNA homologous to the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4, said reduction in expression being determined by comparison with the level of expression in an untransformed soybean.

Claim 57. (currently amended) An RNA comprising:

(a) homology to at least one target mRNA expressed in soybean, and  
(b) two fully complementary RNA regions, which are unrelated to any endogenous RNA in soybean and which are transcribed from SEQ ID NO:13 , comprising at least nucleotides 7-36 and 82-111 or 7-36, 44-73, 82-111 and 119-148 of SEQ ID NO: 13, and which are in proximity to a sequence homologous to all or part of the RNA in (a), wherein the RNA in (a) and (b) , when introduced into soybean, reduces expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with the sequence homologous to all or part of the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 58. (new) An RNA comprising:

(a) homology to at least one target mRNA expressed in soybean,  
(b) an RNA region, which is unrelated to any endogenous RNA in soybean and which is transcribed from SEQ ID NO:13, comprising at least nucleotides 7-36 or 7-36 and 44-73 and is located 5' to a sequence homologous to all or part of the RNA in (a), and  
(c) the reverse complement of (b), comprising at least nucleotides 82-111 or 82-111 and 119-148 and is located 3' to a sequence homologous to all or part of the RNA in (a), wherein the RNA in (a) and (b) , when introduced into the host, reduces the expression of the target mRNA or any endogenous mRNA that has

at least 80% sequence identity with the sequence homologous to all or part of the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 59. (new) A method for reducing expression in soybean of a target mRNA or any endogenous mRNA having at least 80% sequence identity with a sequence homologous to all or part of the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4, the method comprising:

- (a) introducing into soybean any of the RNA of Claims 57 or 58; and
- (b) selecting soybeans which have reduced expression of the target mRNA or any endogenous mRNA having at least 80% sequence identity with the sequence homologous to all or part of the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4, said reduction in expression being determined by comparison with the level of expression in an untransformed soybean.